

SEQUENCE LISTING

<110> Hoechst Schering AgrEvo GmbH
 <120> Nucleic acid molecules encoding wheat enzymes
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 <151> 1998-05-08
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GCGCGCCCCG CGGCAGCAGC AGCACCGCAG TGGGAGAGAG AGGCTTCGCC CCGGCCCCGCA	206
CGGAGGGGG CGATCCACCG TCCGTGCGTC CGCACMCCT CCGCCTCCCTC CCGTGTCCCC	366
CCCGCCCCACA CCC ATG GCG GCG ACG GGC GTC GGC GCC GGG TGC CTC GCC Met Ala Ala Thr Gly Val Gly Ala Gly Cys Leu Ala	315
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CCC AGC GTC CGC CTG CGC GCC GAT CCG GCG ACG GCG GCC CGG GCG TCC Pro Ser Val Arg Ala Asp Pro Ala Thr Ala Ala Arg Ala Ser	363
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GCC TGC GTC GTC CGC GCG CGG CTC CGG CGC TTG GCG CGG GGC CGC TAC Ala Cys Val Val Arg Ala Arg Leu Arg Arg Leu Ala Arg Gly Arg Tyr	411
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65 70 75	
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05034462 2000

GCC GGC GTG GGG GAA CTC GCG CCC GAC CTC CTG CTC GAA GGG ATT GCT
 Ala Gly Val Gly Glu Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala 603
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GAG GAT TCC ATC GAC AGC ATA ATT GTG GCT GCA AGT GAG CAG GAT TCT
 Glu Asp Ser Ile Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser 651
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GAG ATC ATG GAT GCG AAT GAG CAA CCT CAA GCT AAA GTT ACA CGT AGC
 Glu Ile Met Asp Ala Asn Glu Gln Pro Gln Ala Lys Val Thr Arg Ser 699
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CAC CGA GTG ATG GTT GTC ATG CCA AGA TAC TTA AAT GGG TCC TCT GAT
 His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp 843
 175 180 185

AAA AAC TAT GCA AAG GCA TTA TAC ACT GCG AAG CAC ATT AAG ATT CCA
 Lys Asn Tyr Ala Lys Ala Leu Tyr Thr Ala Lys His Ile Lys Ile Pro 891
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TGC TTT GGG GGA TCA CAT GAA GTG ACC TTT TTT CAT GAG TAT AGA GAC
 Cys Phe Gly Gly Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp 939
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AAC GTC GAT TGG GTG TTT GTC GAT CAT CCG TCA TAT CAC AGA CCA GGA
 Asn Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly 987
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AGT TTA TAT GGA GAT AAT TTT GGT GCT TTT GGT GAT AAT CAG TTC AGA
 Ser Leu Tyr Gly Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg 1035
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 Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro 1179
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CCA GAG CTC ATG AGG GAG GAC GTG CAA TTT GTC ATG CTT GGA TCT GGG Pro Glu Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly 480 485 490	1755
GAT CCA ATT TTT GAA GGC TGG ATG AGA TCT ACC GAG TCG AGT TAC AAG Asp Pro Ile Phe Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys 495 500 505	1803

GAT AAA TTC CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC CAC AGA 1851
 Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg
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 Val His Gly Thr Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro
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 Phe Gly Ala Lys Gly Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu
 575 580 585

ACC GTG GAC AAG ATG TTG TGG GCA TTG CGA ACC GCG ATG TCG ACA TTC 2091
 Thr Val Asp Lys Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe
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 Lys Asp His Thr Trp Asp His Ala Pro Ser Ser Thr Ser Arg Ser Ser
 625 630 635

AGT GGG CCT TCG TGG ACC AAC CCT ACG TCA TGT AGA CGG GGA CTG GGG 2235
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TTC CGC GGC CCG GAA GGA TAC CCC TGT ACA TTG CGT TGT CCT GCT ACA 2331
 Phe Arg Gly Pro Glu Gly Tyr Pro Cys Thr Leu Arg Cys Pro Ala Thr
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GTA GAG TCG CAA TGC GCC TGC TTG CTT TGG TTC GCC GGT TCG AGA ACA 2379
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 685 690 695 700

TAT GAC GGC TGT GCT GCT GCG GCG GTG ACA GCT TCG GGT GGA CGA CAG 2427
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ATC AGA AAC CAA CTG GTG ACT CTT TAGCCTTAGT GATTGTGAAG TTTGTTGCCT Ile Arg Asn Gln Leu Val Thr Leu 750 755	2577
TCTGTGTATG TTGTCTTGTC CTTAGCTGAC AAATATTTGA CCTGTTGGAG AATTTTATCT TTGCTGCTGT TTTTTTTTAA TCAAAAGAGG GGGTTTCCTC CGATTTCATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA	2637 2697 2757 2771

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Ser Arg Glu Gly Pro Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala 50 55 60
Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro Pro Pro Ala Pro Ala 65 70 75 80
Gln Ser Pro Ala Pro Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly 85 90 95
Glu Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile 100 105 110
Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp 115 120 125

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Thr Gly Glu Ala Ala Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val
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Cys Gly Ser Leu Pro Ile Ala Leu Ala Ala Arg Gly His Arg Val Met
165 170 175

Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala
180 185 190

Lys Ala Leu Tyr Thr Ala Lys His Ile Lys Ile Pro Cys Phe Gly Gly
195 200 205

Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp
210 215 220

Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly
225 230 235 240

Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu
245 250 255

Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr
260 265 270

Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser
275 280 285.

Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr
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Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly
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Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp
325 330 335

Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala
340 345 350

Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr
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Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr
370 375 380

Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys
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Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn
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Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met
465 470 475 480

Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe
485 490 495

Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg
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Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly
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Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn
530 535 540

Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His Gly Thr
545 550 555 560

Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys
565 570 575

Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys
580 585 590

Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys
595 600 605

Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr Lys Asp His Thr
610 615 620

Trp Asp His Ala Pro Ser Ser Thr Ser Arg Ser Ser Gly Pro Ser
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Trp Thr Asn Pro Thr Ser Cys Arg Arg Gly Leu Gly Arg Ser Lys Cys
645 650 655

Glu Ser Pro Ser Ala Leu Lys Thr Ser Ser Ser Phe Arg Gly Pro
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Glu Gly Tyr Pro Cys Thr Leu Arg Cys Pro Ala Thr Val Glu Ser Gln
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Cys Ala Cys Leu Leu Trp Phe Ala Gly Ser Arg Thr Tyr Asp Gly Cys
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